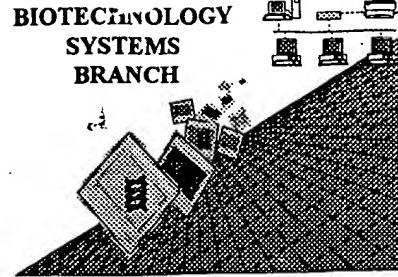


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762,267
Source: Pct/09
Date Processed by STIC: 9/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>**

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,767

DATE: 07/11/2001
TIME: 11:19:54

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07112001\I762767.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

C--> 3 (i) APPLICANT:

4 SCHMIDT, Harald
5 ZABEL, Ulrike
6 POLLER, Wolfgang

W--> 8 (ii) TITLE OF INVENTION: Isolated and purified human soluble
9 guanylyl cyclase al/al (hsGCa1/al)E--> 10 (iii) VOS-101
11 (iv) US 09/762,767

W--> 12 2001-02-13

W--> 13 (iv) PCT/DE99/02601

W--> 14 1999-08-16

W--> 15 (iv) DE 198 37 015.6

W--> 16 1998-08-14

E--> 22 (iii) NUMBER OF SEQUENCES: 10

C--> 24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

C--> 0 (vi) CURRENT APPLICATION DATA:

C--> 0 (A) APPLICATION NUMBER: US/09/762,767

C--> 0 (B) FILING DATE: 13-Feb-2001

ERRORED SEQUENCES

E--> 30 (2) DATA TO SEQ ID NO: 1:

E--> 0 (2) INFORMATION FOR SEQ ID NO:

31 (i) SEQUENCE CHARACTERISTICS:
32 (A) LENGTH: 3015 basepairs
33 (B) TYPE: nucleotide
34 (C) STRANDEDNESS: doublestrand
35 (D) TOPOLOGY: linear
37 (ii) MOLECULE TYPE: genomic DNA
0 (D) DEVELOPMENTAL STAGE: 1:

E--> 39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

41	CCCTTATGGC GATTGGCGG CTGCAGAGAC CAGGACTCAG TTCCCCTGCC CTAGTCTGAG	60
42	CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTCCAGAA GCAGGTTCA GTGCAGAGTT	120
43	TTCCTACACT TTTCCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGCGGAGGAC	180
44	ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGCG TGATCTCACC	240
45	ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG	300
46	GTGTGCGAAG CCACCAAGAC TGCAGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG	360
47	TCTCCGCGCC TGTCTGCACC CTGTCGCCTG AGCTGCCTGA CAGTGACAAT GACATCCCAG	420
48	TTACCAAGTGT CCTTGAATTG ATAGTGGCTT CTGTTGTCA GTCTCATATA AGAACTACAG	480
49	CTCATCAGGA GGAGATCGCA GCAGGGTAAG AGACACCAAC ACCATGTTCT GCACGAAGCT	540

Completely invalid
format for
a U.S.
case.

(See attached)

EPO format is
invalid for U.S.
case

09/762,767 1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

SCHMIDT, Harald
ZABEL, Ulrike
POLLER, Wolfgang

(ii) TITLE OF THE INVENTION: Isolated and purified human soluble guanylyl cyclase a1/g1 (hsGCa1/g1)

(iii) YES-101 →

NUMBER OF SEQUENCES: (insert third and delete all accent marks - they cannot be processed in the CRF)

(vi) US 09/762,767
2001-02-13

goes under CURRENT APPLICATION DATA response in the CRF

(vii) PCT/DE99/02601
1999-08-16

Move program

(viii) DE 198 37 015.6
1998-08-14

These (go under Prior APPLICATION DATA)

(iii) → NUMBER OF SEQUENCES: 10

(j) → COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 ((EPA))

(a) CORRESPONDENCE ADDRESS:
(1) ADDRESSEE:
(2) STREET:
(3) CITY:
(4) STATE:
(5) COUNTRY:
(6) ZIP:

INFORMATION FOR SEQ ID NO: 1: →

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3015 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: doublestrand
- (D) TOPOLOGY: linear

((2) CURRENT APPLICATION DATA:
(1) APPLICATION NUMBER:
(2) FILING DATE:

((3) PRIOR APPLICATION DATA:
(1) APPLICATION NUMBER:
(2) FILING DATE:

→ insert these mandatory fields and responses for a U.S. case

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTTATGGC	GATTGGCGG	CTGCAGAGAC	CAGGACTCAG	TTCCCCTGCC	CTAGTCTGAG	60
CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTCCAGAA	GCAGGTTCA	GTGCAGAGTT	120
TTCCTACACT	TTCCCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGGC	TGATCTCACC	240
ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
TCTCCGCGCC	TGTCTGCACC	CTGTCGCTG	AGCTGCTGA	CAGTGACAAT	GACATCCCAG	420
TTACCACTGT	CCTTGAATTG	ATAGTGGCTT	CTGTTTGTC	GTCTCATATA	AGAACTACAG	480
CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAC	ACCATGTTCT	GCACGAAGCT	540
CAAGGATCTC	AAGATCACAG	GAGAGTGTCC	TTTCTCCTTA	CTGGCACCAAG	GTCAAGTTCC	600
TAACGAGTCT	TCAGAGGAGG	CAGCAGGAAG	CTCAGAGAGC	TGCAAAGCAA	CCGTGCCCAT	660
CTGTCAGAC	ATTCCCTGAGA	AGAACATACA	AGAAAGTCTT	CCTCAAAGAA	AAACCAGTCG	720
GAGCCGAGTC	TATCTTCACA	CTTGGCAGA	GAGTATTGTC	AAACTGATT	TCCCAGAGTT	780
TGAACGGCTG	AATGTTGCAC	TTCAGAGAAC	ATTGGCAAAG	CACAAAATAA	AAGAAAGCAG	840
GAAATCTTG	GAAAGAGAAG	ACTTGAAAAA	AAACAATTGCA	GAGCAAGCAG	TTGCAGCAGG	900
AGTTCAGTG	GAGGTTATCA	AAGAATCTCT	TGGTGAAGAG	GTTTTAAAAA	TATGTTACGA	960
GGAAGATGAA	AACATCCTTG	GGGTGGTTGG	AGGCACCCCTT	AAAGATTTT	AAACACAGCTT	1020

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CAGTACCCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAAGCA	GGAAAAAGGG	GCAGGCTTGA	1080
GGACGCCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATTT	CTACATGTTT	ACTACTTCTT	1140
CCCTAACAGAGA	ACCACCTCCC	TGATTCTTCC	CGGCATCATA	AAGGCAGCTG	CTCACGTATT	1200
ATATGAAACG	GAAGTGGAAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	ATTGCAGCGA	1260
GTTTGTGAAT	CAGCCCTACT	TGTTGTACTC	CGTTCACATG	AAAAGCACCA	AGCCATCCCT	1320
GTCCCCCAGC	AAACCCAGT	CCTCGCTGGT	GATTCCCACA	TCGCTATTCT	GCAAGACATT	1380

delete all hard page
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09/262,767 3

TCCATTCCAT	TTCATGTTG	ACAAAGATAT	GACAATTCTG	CAATTGGCA	ATGGCATCAG	1440
AAGGCTGATG	AACAGGAGAG	ACTTCAAGG	AAAGCCTAAT	TTTGAAGAAT	ACTTTGAAAT	1500
TCTGACTCCA	AAAATCAACC	AGACGTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	1560
TGTTGTACGA	GTGAGGAGAT	GGGACAAC	TGTGAAGAAA	TCTTCAAGGG	TTATGGACTT	1620
CAAAGGCCAA	ATGATCTACA	TTGTTGAATC	CAGTGCAATC	TTGTTTTGG	GGTCACCC	1680
TGTGGACAGA	TTAGAAAGATT	TTACAGGACG	AGGGCTCTAC	CTCTCAGACA	TCCCATTCA	1740
CAATGCACTG	AGGGATGTGG	TCTTAATAGG	GGAACAAGCC	CGAGCTCAAG	ATGGCCTGAA	1800
GAAGAGGCTG	GGGAAGCTGA	AGGCTACCC	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	1860
GAAGAAAAAG	ACAGTAGACC	TTCTGTGCTC	CATATTCCC	TGTGAGGTTG	CTCAGCAGCT	1920
GTGCAAGGG	CAAGTTGTGC	AAGCCAAGAA	GTTCAGTAAT	GTCACCATGC	TCTTCTCAGA	1980
CATCGTTGGG	TTCACTGCCA	TCTGCTCCC	GTGCTCACCG	CTGCAGGTCA	TCACCATGCT	2040
CAATGCACTG	TACACTCGCT	TCGACCAGCA	GTGTGGAGAG	CTGGATGTCT	ACAAGGTGGA	2100
GACCATTGGC	GATGCCTATT	GTGTAGCTGG	GGGATTACAC	AAAGAGAGTG	ATACTCATGC	2160
TGTTCAGATA	GCGCTGATGG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	2220
CCATGGAGAA	CCTATCAAGA	TGCGAATTGG	ACTGCACTCT	GGATCAGTTT	TTGCTGGCGT	2280
CGTTGGAGTT	AAAATGCC	GTTACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2340
ATTTGAGTCC	TGCA	GTCAGTGTAC	CACGAAAAT	CAATGTCAGC	CCAACAACTT	2400
CAAAGACTGT	CCTGGTTTCG	TGTTTACCC	TCGATCAAGG	GAGGAAC	CACCAAAC	2460
CCCTAGTGA	ATCCCCGGAA	TCTGCCATT	TCTGGATGCT	TACCAACAAG	GAACAAAC	2520
AAAACCATGC	TTCCAAAAGA	AAGATGTGGA	AGATGGCAAT	GCCAA	TTAGGCAAAGC	2580
ATCAGGAATA	GATTAGCAAC	CTATATACCT	ATTTATAAGT	CTTGGGGTT	TGACTCATG	2640
AAGATGTGTA	GAGCCTCTGA	AAGCACTTTA	GGGATTGTAG	ATGGCTAAC	AGCAGTATTA	2700
AAATTCAGG	AGCCAAGTCA	CAATCTTCT	CCTGTTAAC	ATGACAA	ATGACTCACTT	2760
CAGTACTTCA	GCTCTTCAAG	AAAAAA	AAACCTTAA	AAGCTACTTT	TGTGGGAGTA	2820
TTTCTATTAT	ATAACCAGCA	CTTACTACCT	GTACTCAAA	TTCAGCAC	TGTACATATA	2880
TCAGATAATT	GTAGTCAATT	GTACAAACTG	ATGGAGTCAC	CTGCAATCTC	ATATCCTGGT	2940
GGAATGCCAT	GGTTATTAAA	GTGTGTTGT	GATAGTGTG	TCAAAAAAA	AAAAAA	3000
AAAAAAAAAA	AAAAAA					3015

(2) DATA TO SEQ ID NO: 2: INFORMATION FOR SEQ ID NO: 2!

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al
(hsGCaI)) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

(xi) SEQUENCEDDESCRIPTION: SEQ ID NO: 2:

Met	Phe	Cys	Thr	Lys	Leu	Lys	Asp	Leu	Lys	Ile	Thr	Gly	Glu	Cys	Pro
							5				10				15
Phe	Ser	Leu	Leu	Ala	Pro	Gly	Gln	Val	Pro	Asn	Glu	Ser	Ser	Glu	Glu
							20			25				30	
Ala	Ala	Gly	Ser	Ser	Glu	Ser	Cys	Lys	Ala	Thr	Val	Pro	Ile	Cys	Gln
							35			40				45	
Asp	Ile	Pro	Glu	Lys	Asn	Ile	Gln	Glu	Ser	Leu	Pro	Gln	Arg	Lys	Thr
							50			55				60	
Ser	Arg	Ser	Arg	Val	Tyr	Leu	His	Thr	Leu	Ala	Glu	Ser	Ile	Cys	Lys
							65			70				75	
Leu	Ile	Phe	Pro	Glu	Phe	Glu	Arg	Leu	Asn	Val	Ala	Leu	Gln	Arg	Thr
							85			90				95	
Leu	Ala	Lys	His	Lys	Ile	Lys	Glu	Ser	Arg	Lys	Ser	Leu	Glu	Arg	Glu
							100			105				110	
Asp	Phe	Glu	Lys	Thr	Ile	Ala	Glu	Gln	Ala	Val	Ala	Ala	Gly	Val	Pro
							115			120				125	
Val	Glu	Val	Ile	Lys	Glu	Ser	Leu	Gly	Glu	Glu	Val	Phe	Lys	Ile	Cys
							130			135				140	
Tyr	Glu	Glu	Asp	Glu	Asn	Ile	Leu	Gly	Val	Val	Gly	Gly	Thr	Leu	Lys
							145			150				155	
Asp	Phe	Leu	Asn	Ser	Phe	Ser	Thr	Leu	Leu	Lys	Gln	Ser	Ser	His	Cys

Follow
these
instructions
throughout

09/762,767 Y

Gln	Glu	Ala	Gly	Lys	Arg	Gly	Arg	Leu	Glu	Asp	Ala	Ser	Ile	Leu	Cys
				165					170					175	
				180					185					190	
Leu	Asp	Lys	Glu	Asp	Asp	Phe	Leu	His	Val	Tyr	Tyr	Phe	Phe	Pro	Lys
				195				200				205			
Arg	Thr	Thr	Ser	Leu	Ile	Leu	Pro	Gly	Ile	Ile	Lys	Ala	Ala	Ala	His
				210			215			220					
Val	Leu	Tyr	Glu	Thr	Glu	Val	Glu	Val	Ser	Leu	Met	Pro	Pro	Cys	Phe
				2225		230			235					240	
His	Asn	Asp	Cys	Ser	Glu	Phe	Val	Asn	Gln	Pro	Tyr	Leu	Leu	Tyr	Ser
				245				250				255			
Val	His	Met	Lys	Ser	Thr	Lys	Pro	Ser	Leu	Ser	Pro	Ser	Lys	Pro	Gln
				260			265			270					
Ser	Ser	Leu	Val	Ile	Pro	Thr	Ser	Leu	Phe	Cys	Lys	Thr	Phe	Pro	Phe
				275			280				285				
His	Phe	Met	Phe	Asp	Lys	Asp	Met	Thr	Ile	Leu	Gln	Phe	Gly	Asn	Gly
				290			300			305					
Ile	Arg	Arg	Leu	Met	Asn	Arg	Arg	Asp	Phe	Gln	Gly	Lys	Pro	Asn	Phe
				310		315			320					325	
Glu	Glu	Tyr	Phe	Glu	Ile	Leu	Thr	Pro	Lys	Ile	Asn	Gln	Thr	Phe	Ser
				330			335					340			
Gly	Ile	Met	Thr	Met	Leu	Asn	Met	Gln	Phe	Val	Val	Arg	Val	Arg	Arg
				345			350				355				
Trp	Asp	Asn	Ser	Val	Lys	Lys	Ser	Ser	Arg	Val	Met	Asp	Leu	Lys	Gly
				360			365				370				
Gln	Met	Ile	Tyr	Ile	Val	Glu	Ser	Ser	Ala	Ile	Leu	Phe	Leu	Gly	Ser
				375			380			385					
Pro	Cys	Val	Asp	Arg	Leu	Glu	Asp	Phe	Thr	Gly	Arg	Gly	Leu	Tyr	Leu
				390		395			400					405	
Ser	Asp	Ile	Pro	Ile	His	Asn	Ala	Leu	Arg	Asp	Val	Val	Leu	Ile	Gly
				410			415					420			
Glu	Gln	Ala	Arg	Ala	Gln	Asp	Gly	Leu	Lys	Lys	Arg	Leu	Gly	Lys	Leu
				425			430				435				
Lys	Ala	Thr	Leu	Glu	Gln	Ala	His	Gln	Ala	Leu	Glu	Glu	Glu	Lys	Lys
				440			445				450				
Lys	Thr	Val	Asp	Leu	Leu	Cys	Ser	Ile	Phe	Pro	Cys	Glu	Val	Ala	Gln
				455			460				465				
Gln	Leu	Trp	Gln	Gly	Gln	Val	Val	Gln	Ala	Lys	Lys	Phe	Ser	Asn	Val
				470		475			480					485	
Thr	Met	Leu	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr	Ala	Ile	Cys	Ser	Gln
				490				495				500			
Cys	Ser	Pro	Leu	Gln	Val	Ile	Thr	Met	Leu	Asn	Ala	Leu	Tyr	Thr	Arg
				505				510				515			
Phe	Asp	Gln	Gln	Cys	Gly	Glu	Leu	Asp	Val	Tyr	Lys	Val	Glu	Thr	Ile
				520			525				530				
Gly	Asp	Ala	Tyr	Cys	Val	Ala	Gly	Gly	Leu	His	Lys	Glu	Ser	Asp	Thr
				535			540				545				
His	Ala	Val	Gln	Ile	Ala	Leu	Met	Ala	Leu	Lys	Met	Met	Glu	Leu	Ser
				550			555			560			565		
Asp	Glu	Val	Met	Ser	Pro	His	Gly	Glu	Pro	Ile	Lys	Met	Arg	Ile	Gly
				570				575				580			
Leu	His	Ser	Gly	Ser	Val	Phe	Ala	Gly	Val	Val	Gly	Val	Lys	Met	Pro
				585				590				595			
Arg	Tyr	Cys	Leu	Phe	Gly	Asn	Asn	Val	Thr	Leu	Ala	Asn	Lys	Phe	Glu
				600			605				610				
Ser	Cys	Ser	Val	Pro	Arg	Lys	Ile	Asn	Val	Ser	Pro	Thr	Thr	Tyr	Arg
				615			620			625					

09/162,767 S

Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu
 630 635 640 645
 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
 650 655 660
 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
 665 670 675
 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly
 680 685 690

Ile Asp
695

(2) DATA TO SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: doublestrand
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCCCCCG	CCGCTGCCGC	CTCTGCCCTGG	GTCCCCTCGG	CCGTACCTCT	CGGTGGGGGC	60
TGCCCTCCCCG	GCTCCCGGTG	CAGACACCAT	GTACGGATTT	GTGAATCACCG	CCCTGGAGTT	120
GCTGGTGATC	CGCAATTACG	GCCCCGAGGT	GTGGGAAGAC	ATCAAAAAAG	AGGCACAGTT	180
AGATGAAGAA	GGACAGTTTC	TTGTCAGAAT	AATATATGAT	GACTCCAAAA	CTTATGATTT	240
GGTTGCTGCT	GCAAGCAAAG	TCCTCAATCT	CAATGCTGGA	GAAATCCTCC	AAATGTTGG	300
GAAGATGTT	TTCGTCTTT	GCCAAGAACATC	TGGTTATGAT	ACAATCTTGC	GTGTCTGGG	360
CTCTAATGTC	AGAGAATTC	TACAGAACCT	TGATGCTCTG	CACGACCACC	TTGCTACCAT	420
CTACCCAGGA	ATGCGTGCAC	CTTCCTTTAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
CATTTGCAC	TACTACTCAG	AGAGAGAAGG	ACTTCAGGAT	ATTGTCAATTG	GAATCATCAA	540
AACAGTGGCA	CAACAAATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTTC	AGCAAAGAAA	600
TGAAGAATGT	GATCATACTC	AATTTTAAT	TGAAGAAAAA	GAGTCAAAAG	AAGAGGATT	660
TTATGAAGAT	CTTGACAGAT	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
TACATTCTGC	AAAGCTTTTC	CTTTTCATAT	AATATTGAC	CGGGACCTAG	TGGTCACTCA	780
GTGTGGCAAT	GCTATATACA	GAGTTCTCCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
GTCTGTCTTC	TCGCTGGTTC	GTCCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTCTCA	900
CATCAAACT	GTTTTGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
ATGTGAGGAT	GAACGTACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
CTACTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTCA	TGAACCTGG	1080
CGATTGACA	AGGAGAGGGC	TGTATCTAACG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
TCTTGTCTT	TTGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCCAAG	AACTGGAAAT	1200
CCTCACTGAC	AGGCTACAGC	TCACGTTAACG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
CACATTGCTG	TATTCTGTCC	TTCCCTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
AGTGCCTGCC	AAAAGATATG	ACAATGTGAC	CATCCTCTT	AGTGGCATTG	TGGGCTTCAA	1380
TGCTTCTGT	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
CGACCTCTAC	ACCAAGATTG	ACACACTGAC	TGATTCCCGG	AAAAACCCAT	TTGTTTATAA	1500
GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAAGAGC	CATGCATTCA	1560
CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
AGTAGATGGT	GAATCTGTT	AGATAACAAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
TGTCATAGGA	CAGCGGATGTC	CTCGATACTG	TCTTTTGGG	AATACTGTCA	ACCTCACAAG	1740
CCGAACAGAA	ACCACAGGGAG	AAAAGGGAAA	AATAAAATGTG	TCTGAATATA	CATACAGATG	1800
TCTTATGTCT	CCAGAAAATT	CAGATCCACA	ATTCCACTG	GAGCACAGAG	GCCCAGTGTG	1860
CATGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTCTA	TCCAGAAAAA	ATACAGGAAC	1920
AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGGATTAT	GGGGTGAAGA	GGAGTACAGA	1980
CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCTTC	CCTATGGATA	2040
CAGATTTCT	TTTGTCTTG	TCCATTACCC	CAAGACTTTC	TTCTAGATAT	ATCTCTCACT	2100
ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTT	AGGCTTTAGT	ATATTATCTA	2160
AAGTTGGCT	TTTGATGTGG	ATGATGTGAG	CTTCATGTGT	CTTAAAATCT	ACTACAAGCA	2220
TTACCTAACAA	TGGTGATCTG	CAAGTAGTAG	GCACCCAATA	AATATTGTT	GAATTTAGTT	2280
AAATGAAACT	GAACAGTGT	TGGCCATGTG	TATATTATA	TCATGTTAC	CAAATCTGTT	2340

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TAGTGTCCA CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AAGTTTATAT
CATGTTGGTG TATATCCTTA TAGAAATCAT TTTCTAAAGG AGT

2400
2443

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1
(hsGCb1))

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn
5 10 15
Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp
20 25 30
Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr
35 40 45
Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly
50 55 60
Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu
65 70 75 80
Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu
85 90 95
Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr
100 105 110
Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly
115 120 125
Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp
130 135 140
Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr
145 150 155 160
Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His
165 170 175
Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr
180 185 190
Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile
195 200 205
Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp
210 215 220
Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu
225 230 235 240
Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu
245 250 255
Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile
260 265 270
Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu
275 280 285
Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu
290 295 300
Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu
305 310 315 320
Phe Leu Cys Ser Pro Ser Val Met Asn Leu Asp Asp Leu Thr Arg Arg
325 330 335
Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
340 345 350
Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
355 360 365
Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu

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370	375	380
Asp Glu Lys Lys Lys	Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro	
385	390	395 400
Ser Val Ala Asn Glu	Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg	
	405	410 415
Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala		
	420	425 430
Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn		
	435	440 445
Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg		
	450	455 460
Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met		
	465	470 475 480
Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile		
	485	490 495
Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val		
	500	505 510
Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val		
	515	520 525
Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly		
	530	535 540
Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly		
	545	550 555 560
Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu		
	565	570 575
Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met		
	580	585 590
Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn		
	595	600 605
Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp		
	610	615

(2) DATA TO SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCa1)

(iii) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro

(2) DATA TO SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCB1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
5 10 15

Thr Gly Thr Glu Glu Thr

(2) DATE TO SEND ID NO. 2

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 28 basepairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single ~~strands~~
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

(2) DATA TO SEQ ID NO: 8:

- ↑
insert
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG

18

(2) DATA TO SEQ ID NO: 9:

- ↑
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

(2) DATA TO SEQ ID NO: 10:

- ↑
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20

- 1) Please ensure all (A) LENGTH responses reflect actual number of bases or amino acids.
- 2) all U.S. applications filed on or after July 1, 1998 and which cannot claim a prior application filed before July 1, 1998, need to be in new Sequence Rule format.